

Applicant: Jay M. Short
Application No.: 10/034,622
Filed: December 21, 2001
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REMARKS

Claims 1-4 were pending before this Preliminary Amendment. By the present communication no claims are added or canceled and claims 1-4 are amended to define Applicant's invention with greater particularity. The amendments add no new matter being fully supported by the specification and original claims. Moreover the amendments are merely cosmetic in nature and do not change the scope of the claimed invention.

Applicant respectfully requests passage of the claims to allowance. In the event any matters remain to be resolved in view of this communication, the Examiner is encouraged to call the undersigned so that a prompt disposition of this application can be achieved.

Respectfully submitted,

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Attachment: Exhibit A

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EXHIBIT A

Version with Markings to Show Changes Made

1. A catalogued nucleic acid library formed from an organism sample comprised of a plurality of organisms, formed by a process comprising the steps of:
 - (a) forming a derived organism sample from an organism sample, such that the proportional representations of the constituents in said derived organism sample are adjusted to advantage by performing in any order, and at least one time, at least one step selected from the group consisting of: (i) subjecting a working organism sample to a process of selection, and (ii) recovering a fraction of a working organism sample having at least one desired characteristic;
 - (b) isolating a[n initial] nucleic acid sample from said derived organism sample; and
 - (c) forming a derived nucleic acid library from said [initial] nucleic acid sample, such that the proportional representations of the constituents in said nucleic acid library are adjusted to advantage by performing in any order, and at least one time, at least one step selected from the group consisting of: (i) subjecting a working nucleic acid sample to a period of selection, (ii) recovering a fraction of a working nucleic acid sample having at least one desired characteristic, and (iii) assembling a working nucleic acid sample into a nucleic acid library[;whereby said nucleic acid library having advantageously adjusted proportional representations of the constituents and having an improved yield potential when said library is screened, is serviceable for identifying a potentially desirable nucleic acid target, particularly when said potentially desirable nucleic acid target is underrepresented an organism source sample, and particularly also when said potentially desirable nucleic acid target is underrepresented a nucleic acid source sample].

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2. (Amended) The catalogued nucleic acid library according to claim 1 wherein the step of [(b)] isolating a nucleic acid sample [from said derived organism sample is comprised of] comprises isolating genomic DNA[,]; and wherein the step of [(c)] forming a derived nucleic acid library [from said initial nucleic acid sample is comprised of] comprises forming a genomic DNA library, such that a catalogued genomic DNA library is formed.

3. (Amended) The catalogued nucleic acid library according to claim 1 wherein the step of [(b)] isolating a nucleic acid sample [from said derived organism sample is comprised of] comprises isolating genomic gene cluster DNA[,]; and wherein the step of [(c)] forming a derived nucleic acid library [from said initial nucleic acid sample is comprised of] comprises forming a genomic gene cluster DNA library, such that a catalogued genomic gene cluster DNA library is formed.

4. (Amended) The catalogued nucleic acid library according to claim 1 wherein the step of [(b)] isolating a nucleic acid sample [from a derived organism sample is comprised of] comprises isolating RNA[,]; and wherein the step of [(c)] forming a derived nucleic acid library [from said initial nucleic acid sample is comprised of] comprises forming a cDNA library, such that a catalogued cDNA library is formed.